

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/227,742

DATE: 04/12/1999
TIME: 13:20:38

INPUT SET: S31428.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information

(i) APPLICANT: BLOOM, FREDERIC .
KUO, JONATHAN
LIN, JHY-JHU
MA, JIN

(ii) TITLE OF THE INVENTION: METHOD FOR INCREASING VIABILITY
AND TRANSFORMATION EFFICIENCY OF BACTERIA DURING
STORAGE AT LOW TEMPERATURES

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Howrey & Simon
(B) STREET: 1299 Pennsylvania Avenue, N.W.
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20004-2402

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/227,742
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/826,426
(B) FILING DATE: 27-MAR-1997
(A) APPLICATION NUMBER: U.S. Ser. No. 60/025,838
(B) FILING DATE: 05-SEP-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Auerbach, Jeffrey
(B) REGISTRATION NUMBER: 32,680
(C) REFERENCE/DOCKET NUMBER: 04227-0031

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47
48 (ix) TELECOMMUNICATION INFORMATION:
49 (A) TELEPHONE: 202 383-7451
50 (B) TELEFAX: 202 383-6610
51 (C) TELEX:
52
53
54 (2) INFORMATION FOR SEQ ID NO:1:
55
56 (i) SEQUENCE CHARACTERISTICS:
57 (A) LENGTH: 25 base pairs
58 (B) TYPE: nucleic acid
59 (C) STRANDEDNESS: single
60 (D) TOPOLOGY: linear
61
62
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65 CGACTCACTA TAGGGAAGTG ATCCT 25
66
67 (2) INFORMATION FOR SEQ ID NO:2:
68
69 (i) SEQUENCE CHARACTERISTICS:
70 (A) LENGTH: 25 base pairs
71 (B) TYPE: nucleic acid
72 (C) STRANDEDNESS: single
73 (D) TOPOLOGY: linear
74
75
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
77
78 GATTTAGGTG AACTATAGA GATCC 25
79
80 (2) INFORMATION FOR SEQ ID NO:3:
81
82 (i) SEQUENCE CHARACTERISTICS:
83 (A) LENGTH: 23 base pairs
84 (B) TYPE: nucleic acid
85 (C) STRANDEDNESS: single
86 (D) TOPOLOGY: linear
87
88
89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
90
91 CCACATATCC GGGTTTTTCG CTG 23
92
93 (2) INFORMATION FOR SEQ ID NO:4:
94
95 (i) SEQUENCE CHARACTERISTICS:
96 (A) LENGTH: 23 base pairs
97 (B) TYPE: nucleic acid
98 (C) STRANDEDNESS: single
99 (D) TOPOLOGY: linear

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100
101
102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
103
104 GAGGTTGGCA GGTGTATGG AGT
105
106 23
107 (2) INFORMATION FOR SEQ ID NO:5:
108 (i) SEQUENCE CHARACTERISTICS:
109 (A) LENGTH: 23 base pairs
110 (B) TYPE: nucleic acid
111 (C) STRANDEDNESS: single
112 (D) TOPOLOGY: linear
113
114
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
116
117 TATGGAGCAG GCAATCGCTG ATG
118
119 23
120 (2) INFORMATION FOR SEQ ID NO:6:
121 (i) SEQUENCE CHARACTERISTICS:
122 (A) LENGTH: 23 base pairs
123 (B) TYPE: nucleic acid
124 (C) STRANDEDNESS: single
125 (D) TOPOLOGY: linear
126
127
128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
129
130 CGTGAAGTGT TCGGCGATAA GAG
131
132 23
133 (2) INFORMATION FOR SEQ ID NO:7:
134 (i) SEQUENCE CHARACTERISTICS:
135 (A) LENGTH: 23 base pairs
136 (B) TYPE: nucleic acid
137 (C) STRANDEDNESS: single
138 (D) TOPOLOGY: linear
139
140
141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
142
143 AATGCGGCCT CCGGCACTAA CAC
144
145 23
146 (2) INFORMATION FOR SEQ ID NO:8:
147 (i) SEQUENCE CHARACTERISTICS:
148 (A) LENGTH: 23 base pairs
149 (B) TYPE: nucleic acid
150 (C) STRANDEDNESS: single
151 (D) TOPOLOGY: linear
152

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153
154
155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
156 GGTACGGTG CGTTGGCAGG ATT
157
158 (2) INFORMATION FOR SEQ ID NO:9: 23
159
160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 23 base pairs
162 (B) TYPE: nucleic acid
163 (C) STRANDEDNESS: single
164 (D) TOPOLOGY: linear
165
166
167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
168 TATCAACGCC ATGCATCGCC ATC
169
170 (2) INFORMATION FOR SEQ ID NO:10: 23
171
172 (i) SEQUENCE CHARACTERISTICS:
173 (A) LENGTH: 23 base pairs
174 (B) TYPE: nucleic acid
175 (C) STRANDEDNESS: single
176 (D) TOPOLOGY: linear
177
178
179 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
180 ACTCCATACA ACCTGCCAAC CTC
181
182 (2) INFORMATION FOR SEQ ID NO:11: 23
183
184 (i) SEQUENCE CHARACTERISTICS:
185 (A) LENGTH: 17 base pairs
186 (B) TYPE: nucleic acid
187 (C) STRANDEDNESS: single
188 (D) TOPOLOGY: linear
189
190
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
192 CTGGCGGCGG CGAAGAG
193
194 (2) INFORMATION FOR SEQ ID NO:12: 17
195
196 (i) SEQUENCE CHARACTERISTICS:
197 (A) LENGTH: 21 base pairs
198 (B) TYPE: nucleic acid
199 (C) STRANDEDNESS: single
200 (D) TOPOLOGY: linear
201
202
203
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205

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

206
207
208 AAATGGCTGA TCGGACTTGT T
209

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

219
220
221 TCCGGGGTGT CGTTGTATT
222

19

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

234 CGTAGNTTTC GTTNCATTGG CCCTCAAACC CCTAATAGCG CCAGCGACAA CAACGCGCTG 60
235 GCAATACCAC CGCCGATAAT CGCCGCTTCC CGTTTGCTGC TGCCCGTGCG GTTAAACCAC 120
236 GGCGCGGAGC AGGGGAGCGG TAATGTCTGT TCCATCACCC CGCAAAGCAT TTCCCGTTTG 180
237 CGCCCAAAGC CCTTACGTTT TTGCATCGTG AATCCGGCGT CCTGCAAACC GCGGCGGACA 240
238 AAACCGGCAG ACGTAAATGT CGCCAGCGTG CCGCCCGGAC GCGCCAAACCT TGCCATGGCG 300
239 TTAAACAGAT TTTGCGTCCA CATATCCGGG TCCAGTTGGC GCGCAAAGCC GTCCAGAAAC 360
240 CAGGCATCTA CTTTTTGATT TAGCGAATCG TCCAGTTGGC TGGTCAGTTC GTTAATATCG 420
241 CCAAACCATA AATCCAGCGT CACGCGGCCT TCATCGAGCA ATAAACGATG GCAACCGGGC 480
242 AAGGGCATTG GCCACTGCGC CTGAAGTTGT TCTGCCCACG GAGCCAGTTC CGGCCAGTGT 540
243 TGATGCGCTA AGGCTAAATC CGCACGGGTG AGGGGAAATT TCTCAAAACT AATGAAATGT 600
244 AAGCGTTGTA ATTGCGCTTG CGGATGCGCT TCGCGAAACT GATCAAATGC CTGCCATAGC 660
245 GTCAGGAAGT TTAATCCGGT GCCGAAGCCG CTCTCTGCTA CCACAAACAG AGGATGTGGA 720
246 TGCTCAGGAA AGCGTACCTC TAATTGGTTG CCTCCCAGAA AAACATAACG CGTCTCTTCC 780
247 AGCCCGTTAT CGTTGGAAAA ATAGACATCG TCAAAATCTC GGGAAACAGG TGTACCCTCA 840
248 GCATTAAATT CGAGGTGGC AGGTTGTATG GAGTAGTGT TCACGTAAGT TACTCGTCTT 900
249 ACAGGCGGTG GCTCGATCTT AGCGATGTGT GTAAGGCTGC GCAAATTTCT CTATTAAATG 960
250 GCTGATCGGA CTTGTTCCGG GTACAAGTGT ACGCTATTGT GCATTTCGAAA CTTACTCTAT 1020
251 GTGCGACTTA CAGAGGTATT GAATGAAACG TGCAGTGATT ACTGGCCTGG GCATTGTTTC 1080
252 CAGCATCGGT AATAACCAGC AGGAAGTCCT GGCATCTCTG CGTGAAGGAC GTTCAGGGAT 1140
253 CACTTTCTCT CAGGAGCTGA AGGATTCCGG CATGCGTAGC CACGTCTGGG GCAACGTAAA 1200
254 ACTGGATACC ACTGGCCTCA TTGACCGCAA AGTTGTGCGC TTTATGAGCG ACGCATCCAT 1260
255 TTATGCATTC CTTTCTATGG AGCAGGCAAT CGCTGATGCG GGCTCTCTC CGGAAGCTTA 1320
256 CCAGAATAAC CCGCGCGTTG GCCTGATTGC AGTTCCGGC GGCGGCTCCC CGCGTTTCCA 1380
257 GGTGTTTCGG GCTGACGCAA TGCGCGGCCG GCGCGGCTG AAAGCGGTTG GCCCGTATGT 1440
258 GGTCACCAAA GCGATGGCAT CCGGCGTTTC TGCCTGCCTC GCCACCCCGT TTTAAATTC 1500

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SEQUENCE VERIFICATION REPORT
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Original Text